



741179.ST25.txt
SEQUENCE LISTING

<110> Wang, Jin-Town
Lin, Tzu-Lung

<120> A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF

<130> P/741-179

<140> 10/796,669

<141> 2004-03-09

<160> 5

<170> PatentIn version 3.2

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<213> Helicobacter pylori

<400> 1

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<211> 1617

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<222> (1)..(1617)

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1 5 10 15	
cga aac cct aaa aga ata gga caa ttt tta gct gtt tta gga aag ttt	96
Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu Gly Lys Phe	
20 25 30	
gaa aat caa atc ctt aaa tct tca ata atc atg caa att atc aaa tcc	144
Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser	
35 40 45	
gtt ttg gct cat agg ctt tat aga cct act tct ctc aat caa aat aaa	192
Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys	
50 55 60	
gaa ttg aaa gaa aaa ttt gac tcc aat gaa tat gtc ttt agc gat gaa	240
Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu	
65 70 75 80	
gag tta gaa cgc att ata gaa ata tcc cca caa aat cat aaa gaa atg	288
Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met	
85 90 95	
ggc ttt gag cat gga tgg gaa agc cgg ttt gac act tgg tat aag ctt	336
Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu	
100 105 110	

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atg tgt gag ttt ggt ttt tgc tac tat gca aaa tat gag aaa ata ctc Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu 115 120 125	384
atc agc gat agc gct aag atg ctt att ctt gct tat tac aat aaa gaa Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu 130 135 140	432
aac gat gct ttt aaa gaa agc gtt gat gaa agc gta gtt ggg gct ata Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile 145 150 155 160	480
ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct tac aaa aag Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys 165 170 175	528
aat tta aac cat aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys 180 185 190	576
cga ctc aaa aat gcc cat cta acc ccc cta tct gtc aaa gaa atc cct Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro 195 200 205	624
att tta ctt tgt tgg aaa gac gat aac gct aat ggg ctt tat gac tac Ile Leu Cys Trp Lys Asp Asn Ala Asn Gly Leu Tyr Asp Tyr 210 215 220	672
att att cgt tta aga caa gaa atc gtt act atc aat aaa aca gaa ttc Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe 225 230 235 240	720
agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa ctt tta gaa Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu 245 250 255	768
agt gtt aat aaa aca cga ttt aaa atg agc caa atc act aac gaa gcc Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala 260 265 270	816
gtt gat gaa tac att aga aaa atg cgt att aca gga ctt att tca ttg Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu 275 280 285	864
cgt ggt aat ggt agg ttt att gat att aat act aat gaa aat aat aaa Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys 290 295 300	912
ata gat tac att tta caa acc cat aag gct ttt aaa ggg gat tat tta Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu 305 310 315 320	960
aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac atg gcg atc Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile 325 330 335	1008
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gtt aaa tca agc aaa ttg aat gaa cta gca aac act tat act aaa gat Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp 1104	

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355	360	365	
ttt atc aag caa gaa tta ctc att act tgt aac aag caa gaa tca aaa Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys 370 375 380			1152
gat agt ttt tta aga ctc att gat aaa cct tta cgc tta gaa ttt tta Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu 385 390 395 400			1200
agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc gtg ata ccc Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro 405 410 415			1248
aat tat aaa agc gat gat gaa ggc ttg ccc gta tac aca gca agc ggt Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly 420 425 430			1296
aat aaa cct gat att gta gct atg gac aca aaa gcc caa agt tat ata Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile 435 440 445			1344
gaa gtg agc ttg att aga gac aga agt caa agt acc ttg gaa atg ata Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile 450 455 460			1392
cct att gcc aga cat tta aaa gaa ttg att aaa aat agc acc gat att Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile 465 470 475 480			1440
aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat gat gat gcc Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala 485 490 495			1488
aaa gaa tat gcg gaa ttt gcc caa ttc aaa gac aat att aat ata tgt Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys 500 505 510			1536
tgt tat gct att aat gat ttt atc aaa aaa gta gaa aac agc ata gaa Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu 515 520 525			1584
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Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu Gly Lys Phe
 20 25 30

Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser
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35

40

45

Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys
 50 55 60

Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu
 65 70 75 80

Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met
 85 90 95

Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu
 100 105 110

Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu
 115 120 125

Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu
 130 135 140

Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile
 145 150 155 160

Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys
 165 170 175

Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys
 180 185 190

Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro
 195 200 205

Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr
 210 215 220

Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe
 225 230 235 240

Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu
 245 250 255

Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala
 260 265 270

Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu
 275 280 285

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Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys
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Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu
 305 310 315 320

Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile
 325 330 335

Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser
 340 345 350

Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp
 355 360 365

Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys
 370 375 380

Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu
 385 390 395 400

Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro
 405 410 415

Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly
 420 425 430

Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile
 435 440 445

Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile
 450 455 460

Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile
 465 470 475 480

Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala
 485 490 495

Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys
 500 505 510

Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu
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 ttt aat caa gct tta aag cta gaa gaa aat tat ttt agc caa cat ttt 96
 Phe Asn Gln Ala Leu Lys Leu Glu Glu Asn Tyr Phe Ser Gln His Phe
 20 25 30
 agc aac aag ttt ttc agc tat aaa gat tgt gtc aaa atc ggt agc att 144
 Ser Asn Lys Phe Phe Ser Tyr Lys Asp Cys Val Lys Ile Gly Ser Ile
 35 40 45
 aga gag cat ata gaa agc tta aac tta gat aaa tta aat aaa gat att 192
 Arg Glu His Ile Glu Ser Leu Asn Leu Asp Lys Leu Asn Lys Asp Ile
 50 55 60
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 Leu Leu Thr Ser Leu Ile Tyr Ser Met Asp Lys Ile Ala Asn Thr Val
 65 70 75 80
 ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa gat aga ttt 288
 Gly His Tyr Glu Ala Tyr Arg Lys Lys Glu Ile Leu Gln Asp Arg Phe
 85 90 95
 att ttt gag ctt att agc cct ata aaa cat gat aaa aat atc atg ata 336
 Ile Phe Glu Leu Ile Ser Pro Ile Lys His Asp Lys Asn Ile Met Ile
 100 105 110
 gag aga aaa aac gct aac gaa ttg gct aaa acc tta aaa ata gac tta 384
 Glu Arg Lys Asn Ala Asn Glu Leu Ala Lys Thr Leu Lys Ile Asp Leu
 115 120 125
 gtc ttt att gat cct cca tac aat tca agg caa tac agc cgg ttt tat 432
 Val Phe Ile Asp Pro Pro Tyr Asn Ser Arg Gln Tyr Ser Arg Phe Tyr
 130 135 140
 cat ctc tat gaa aac cta gtg cag tgg aaa aaa ccc aaa ctc tat gga 480
 His Leu Tyr Glu Asn Leu Val Gln Trp Lys Lys Pro Lys Leu Tyr Gly
 145 150 155 160
 aca gct tta aag cca tca tgc gag aac atg agc gaa tat tgc cgc tct 528
 Thr Ala Leu Lys Pro Ser Cys Glu Asn Met Ser Glu Tyr Cys Arg Ser
 165 170 175
 aat gcc aag aaa gaa ttg agc gat tta att gaa aaa cta gat tgt aaa 576
 Asn Ala Lys Lys Glu Leu Ser Asp Leu Ile Glu Lys Leu Asp Cys Lys
 180 185 190
 agg att gct tta act tat aat aat acc tat aac tct aag tct agc tct 624
 Arg Ile Ala Leu Thr Tyr Asn Asn Thr Tyr Asn Ser Lys Ser Ser Ser
 195 200 205

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aaa gga aaa tta agc gtt aaa gaa aag gct cat agt ttt ttt aat tca 720
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 225 230 235 240

gga aaa act gat ttt aaa gag cat aaa gaa ttt tta ttt ata gtg gaa 768
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 Glu Pro Phe Val Gly Gly Gly Ser Val Phe Leu Asn Thr Lys Ala Lys
 20 25 30

aga tac tta gct aat gac ata gat act aat att atc aat tta cat aaa 144
 Arg Tyr Leu Ala Asn Asp Ile Asp Thr Asn Ile Ile Asn Leu His Lys
 35 40 45

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cct gat gaa tta aaa aaa caa tat ata aaa act tac tac gcc aaa tac 288
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 85 90 95

aat aaa ata gct tat gaa aaa cta agg gct gat ttt aac tcc aat caa 336
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 100 105 110

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 115 120 125

atg att aga ttt aat tct aaa ggg ctt ttt aat tta cct gtg ggt aat 432
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 130 135 140

741179.ST25.txt

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gat aat gag ata gcc tta tat ggt gtt tta gat agc cta gat aaa aag Asp Asn Glu Ile Ala Leu Tyr Gly Val Leu Asp Ser Leu Asp Lys Lys 210 215 220	672
gga gtt tta ttt ggt ata act aat ctt att tat cac aag gga gag act Gly Val Leu Phe Gly Ile Thr Asn Leu Ile Tyr His Lys Gly Glu Thr 225 230 235 240	720
aat ttt att tta aaa gaa tgg gct aaa aaa tat tat att ttt aat atc Asn Phe Ile Leu Lys Glu Trp Ala Lys Lys Tyr Tyr Ile Phe Asn Ile 245 250 255	768
aaa agt aat tat atc agt tat aat gac aat act att aaa gaa gat agt Lys Ser Asn Tyr Ile Ser Tyr Asn Asp Asn Thr Ile Lys Glu Asp Ser 260 265 270	816
caa gaa atc ttt gta act aat tat agg tga Gln Glu Ile Phe Val Thr Asn Tyr Arg 275 280	846